

VERSION WITH MARKINGS TO SHOW CHANGES MADE

(Added material is noted in bold underline; [deleted material] is noted in brackets)

In the Specification:

Please replace the paragraph beginning on page 4, line 17, with the following rewritten paragraph:

--OPGL is synthesised as a type II transmembrane protein consisting of 317 amino acid residues (human, cf. SEQ ID NO: 2 (corresponding DNA sequence in SEQ ID NO: 1)) or 316 amino acid residues (murine, cf. SEQ ID NOS: 4 and 6 (corresponding DNA sequences in SEQ ID NOS: 3 and 5, respectively)). Alignment of the two amino acid sequences show that identical amino acid residues are found at 87% of the homologous positions.--

Please replace the paragraph beginning on page 24, line 20, with the following rewritten paragraph:

--The promiscuous epitope can according to the invention be a naturally occurring human T-cell epitope such as epitopes from tetanus toxoid (e.g. the P2 and P30 epitopes (SEQ ID NOS: 34 and 35, respectively)), diphtheria toxoid, Influenza virus hemagglutinin (HA), and *P. falciparum* CS antigen. --

Please replace the paragraph beginning on page 25, line 31, with the following rewritten paragraph:

--One especially preferred PADRE peptide is the one having the amino acid sequence AKFVAAWTLKAAA (**SEQ ID NO: 36**) or an immunologically effective subsequence thereof. This, and other epitopes having the same lack of MHC restriction are preferred T-cell epitopes which should be present in the OPGL analogues used in the inventive method. Such super-promiscuous epitopes will allow for the most simple embodiments of the invention wherein only one single modified OPGL is presented to the vaccinated animal's immune system.--

Please replace the paragraph beginning on page 54, line 18, with the following rewritten paragraph:

--A synthetic cDNA encoding the murine OPGL residues 158-316 has been synthesized removing sub-optimal *Eschericia coli* and *Pichia pastoris* codons from the published sequence. Additionally, an N-terminal Histidine tag, part of the cleavage site of the alpha mating factor signal sequence from *Sacharomyces cerevisiae*, and suitable restriction enzymes have been incorporated into the open reading frame (cf. SEQ ID NO: 7 corresponding amino acid sequence in SEQ ID NO: 8).--

Please replace the paragraph beginning on page 54, line 25, with the following rewritten paragraph:

--This cDNA encoding wild type murine OPGL has been cloned into a standard *Eschericia coli* expression vector (pTrc99a) using *Bsp*HI and *Hind*III restriction enzymes and a standard cloning vector (pBluescript KS+) using

SacI and *KpnI* restriction enzymes (yielding SEQ ID NO: 9 (corresponding amino acid sequence in SEQ ID NO: 10)).--

Please replace the paragraph beginning on page 58, line 5, with the following rewritten paragraph:

--PCR of SEQ ID NO: 9 was performed using SEQ ID NOS: 22 and 25 as primers. The resulting PCR fragment was restriction digested with *SacII* and *KpnI* and subsequently purified from an agarose gel. A second PCR using SEQ ID NO: 9 as template was performed using primer SEQ ID NO: 26 and a vector specific primer. The resulting PCR fragment was restriction digested with *KpnI* and *HindIII*. Both fragments were then ligated to SEQ ID NO: 9 in pBluescript KS+ restriction digested with *SacII* and *HindIII*. To correct a single base mutation in this construct, PCR using the construct as template was performed with primers SEQ ID NOS: 33 and 29. The resulting PCR fragment was restriction digested with *PstI* + *EcoRI*, gel purified and subsequently ligated to the erroneous construct digested with *PstI* and *EcoRI*. The verified construct (SEQ ID NO: 13 (corresponding amino acid sequence in SEQ ID NO: 14)) was then transferred to pTrc99a using *BspHI* and *HindIII* restriction enzymes.--

Please replace the paragraph beginning on page 58, line 23, with the following rewritten paragraph:

--PCR was performed using primers SEQ ID NOS: 27 and 28 without template. The resulting PCR fragment was restriction digested with *PstI* and *EcoRI* and subsequently purified from an agarose gel. The resulting fragment was then ligated to SEQ ID NO: 9 in pBluescript KS+ restriction digested with

SacII and *HindIII*. The verified construct (SEQ ID NO: 15 (corresponding amino acid sequence in SEQ ID NO: 16)) was subsequently transferred to pTrc99a using *BspHI* and *HindIII* restriction enzymes.--

Please replace the paragraph beginning on page 59, line 1, with the following rewritten paragraph:

--PCR of SEQ ID NO: 9 was performed using primers SEQ ID NOs: 22 and 29. The resulting PCR fragment was restriction digested with *PstI* and *BstBI* and subsequently purified from an agarose gel. A second PCR using SEQ ID NO: 9 as template was performed using primer SEQ ID NO: 30 and a vector specific primer. The resulting PCR fragment was restriction digested with *BstBI* and *KpnI* and subsequently gel purified. Both fragments were then ligated to SEQ ID NO: 9 in pBluescript KS+ restriction digested with *PstI* and *KpnI*. The verified construct (SEQ ID NO: 17 (corresponding amino acid sequence in SEQ ID NO: 18)) was then transferred to pTrc99a using *BspHI* and *HindIII* restriction enzymes.--

Please replace the paragraph beginning on page 59, line 14, with the following rewritten paragraph:

--PCR of SEQ ID NO: 9 was performed using primers SEQ ID NOs: 22 and 23. The resulting PCR fragment was restriction digested with *SacII* and *KpnI* and subsequently purified from an agarose gel. A second PCR using SEQ ID NO: 9 as template was performed using primer SEQ ID NOs: 24 and 31. The PCR fragment was restriction digested with *KpnI* and *EcoRI* and subsequently gel purified. Both fragments were then ligated to SEQ ID NO: 9 in

pBluescript KS+ restriction digested with *Sac*II and *Eco*RI. The verified construct (SEQ ID NO: 19 (corresponding amino acid sequence in SEQ ID NO: 20)) was then transferred to pTrc99a using *Bsp*HI and *Hind*III restriction enzymes.-

In the Claims:

Please replace Claim 12 with the following amended claim:

Claim 12 (amended) --The method according to claim 11, wherein the natural T-cell epitope is selected from a Tetanus toxoid epitope such as P2 or P30 (SEQ ID NOS: 34 and 35, respectively), a diphtheria toxoid epitope, an influenza virus hemagglutinin epitope, and a *P. falciparum* CS epitope.--



SEQUENCE LISTING

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HALKIER, Torben
HAANING, Jesper

<120> Method for Down-Regulating Osteoprotegerin Ligand Activity

<130> 3631-0108P

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<141> 2001-03-14

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tgtacagggtt gtgtatatgt aaagtccata ggtgatgtt gattcatggt gattacacaa	1320
cgggtttaca atttttaat gatttcctag aattgaacca gattgggaga ggtattccga	1380
tgcttatgaa aaacttacac gtgagctatg gaagggggtc acagtctctg ggtctaacc	1440
ctggacatgt gccactgaga accttgaat taagaggatg ccatgtcatt gcaaagaaat	1500
gatagtgtga agggtaatgt tcttttaatg tgttacattt cgctgggacc tgcaaataag	1560
ttctttttt ctaatgagga gagaaaaata tatgtatTTT tatataatgt ctaaagttat	1620
atttcaggtg taatgtttt tttgttgc tatgttgc tatagtattt	1680
gattcaaat atttaaaaat gtctactgt tgacatattt aatgttttaa atgtacagat	1740
gtatTTTact ggtgcacttt gtaattcccc tgaaggtaact cgtagctaag gggcagaat	1800
actgtttctg gtgaccacat gtatTTTatt tcttttattt tttaactt atagagtctt	1860
cagacttgc aaaactatgc aagcaaaata aataaataaa aataaaatga ataccctgaa	1920
taataagttag gatgttggtc accaggtgcc tttcaattt agaagctaatt tgactttagg	1980
agctgacata gccaaaaagg atacataata ggctactgaa atctgtcagg agtattttat	2040
caattattga acaggtgtct ttttttacaa gagctacaaa ttgttaattt tgtttcttt	2100
ttttccata gaaaatgtac tatagtttat cagccaaaaa acaatccact tttaattt	2160
gtgaaagtta ttttattata ctgtacaata aaagcattgt ctctgaatgt taatTTT	2220
gtacaaaaaaa taaatttgta cgaaaacctg aaaaaaaaaa aaaaaaaggc cggccgctct	2280
agaggccctt attctata	2299

<210> 6
<211> 316
<212> PRT
<213> Mus musculus

<400> 6
Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu
1 5 10 15
Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro
20 25 30
Ala Pro Ser Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser

35	40	45
Met Phe Leu Ala Leu Leu Gly	Leu Gly Leu Gly Gln Val Val Cys Ser	
50	55	60
Ile Ala Leu Phe Leu Tyr	Phe Arg Ala Gln Met Asp Pro Asn Arg Ile	
65	70	75
Ser Glu Asp Ser Thr His Cys	Phe Tyr Arg Ile Leu Arg Leu His Glu	80
85	90	95
Asn Ala Gly Leu Gln Asp Ser Thr	Leu Glu Ser Glu Asp Thr Leu Pro	
100	105	110
Asp Ser Cys Arg Arg Met Lys	Gln Ala Phe Gln Gly Ala Val Gln Lys	
115	120	125
Glu Leu Gln His Ile Val Gly	Pro Gln Arg Phe Ser Gly Ala Pro Ala	
130	135	140
Met Met Glu Gly Ser Trp	Leu Asp Val Ala Gln Arg Gly Lys Pro Glu	
145	150	155
Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser		160
165	170	175
Gly Ser His Lys Val Thr Leu Ser	Ser Trp Tyr His Asp Arg Gly Trp	
180	185	190
Ala Lys Ile Ser Asn Met Thr	Leu Ser Asn Gly Lys Leu Arg Val Asn	
195	200	205
Gln Asp Gly Phe Tyr Tyr	Leu Tyr Ala Asn Ile Cys Phe Arg His His	
210	215	220
Glu Thr Ser Gly Ser Val Pro	Thr Asp Tyr Leu Gln Leu Met Val Tyr	
225	230	235
Val Val Lys Thr Ser Ile Lys	Ile Pro Ser Ser His Asn Leu Met Lys	
245	250	255
Gly Gly Ser Thr Lys Asn Trp	Ser Gly Asn Ser Glu Phe His Phe Tyr	
260	265	270
Ser Ile Asn Val Gly Gly	Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile	
275	280	285
Ser Ile Gln Val Ser Asn Pro	Ser Leu Leu Asp Pro Asp Gln Asp Ala	
290	295	300
Thr Tyr Phe Gly Ala Phe	Lys Val Gln Asp Ile Asp	
305	310	315

<210> 7
<211> 564
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(564)

<220>
<223> Description of Artificial Sequence: Synthetic PCR
product with optimum codons for E. coli and P.
pastoris expression

<220>
<221> misc_binding
<222> (43)..(84)
<223> His tag

<220>

<221> misc_feature
 <222> (1)..(36)
 <223> C-terminal part of *Saccharomyces cerevisiae*
 alpha-mating factor

<220>
 <221> misc_feature
 <222> (85)..(561)
 <223> Encoding wild type murine OPGL, residues 158-316

<400> 7

gag ctc gga tcc ctc gag aaa aga gag gct gaa gct cat gtc atg aaa	48
Glu Leu Gly Ser Leu Glu Lys Arg Glu Ala Glu Ala His Val Met Lys	
1 5 10 15	
cac caa cac caa cat caa cat caa cat caa aaa cct gaa gct	96
His Gln His Gln His Gln His Gln His Gln Lys Pro Glu Ala	
20 25 30	
cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct tct ggt	144
Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly	
35 40 45	
tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt tgg gct	192
Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala	
50 55 60	
aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt aac cag	240
Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln	
65 70 75 80	
gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aga cat cac gaa	288
Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu	
85 90 95	
acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt tac gtt	336
Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val	
100 105 110	
gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg aaa ggt	384
Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly	
115 120 125	
ggt tct acc aaa aac tgg tct ggt aac tct gaa ttc cat ttc tac tct	432
Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser	
130 135 140	
atc aac gtt ggt ttc ttc aaa ctg aga gct ggt gaa gaa atc tct	480
Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser	
145 150 155 160	
atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac gct acc	528
Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr	
165 170 175	
tac ttc ggg gcc ttc aaa gtt cag gac atc gac tag	564
Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp	
180 185	

<210> 8
 <211> 187
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic PCR
 product with optimum codons for *E. coli* and *P.*

pastoris expression

<400> 8
Glu Leu Gly Ser Leu Glu Lys Arg Glu Ala Glu Ala His Val Met Lys
1 5 10 15
His Gln His Gln His Gln His Gln His Gln Lys Pro Glu Ala
20 25 30
Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly
35 40 45
Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala
50 55 60
Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln
65 70 75 80
Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu
85 90 95
Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val
100 105 110
Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly
115 120 125
Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser
130 135 140
Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser
145 150 155 160
Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr
165 170 175
Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
180 185

<210> 9
<211> 519
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DNA encoding
murine OPGL, residues 158-316, fused to His tag

<220>
<221> CDS
<222> (1)..(519)

<220>
<221> misc_binding
<222> (1)..(42)
<223> His tag

<220>
<221> misc_feature
<222> (43)..(519)
<223> Murine OPGL, residues 158-316

<400> 9
atg aaa cac caa cac caa cat caa cat caa cat caa aaa cct 48
Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro
1 5 10 15
gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct 96

Glu	Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Ala	Ser	Ile	Pro	
20																30
tct	ggt	tct	cat	aaa	gtt	acc	ctg	tct	tct	tgg	tat	cac	gac	cgc	ggt	144
Ser	Gly	Ser	His	Lys	Val	Thr	Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly	
35															45	
tgg	gct	aaa	atc	tct	aac	atg	acc	ctg	tct	aac	ggt	aaa	ctg	aga	gtt	192
Trp	Ala	Lys	Ile	Ser	Asn	Met	Thr	Leu	Ser	Asn	Gly	Lys	Leu	Arg	Val	
50															60	
aac	cag	gac	ggt	ttc	tac	tac	ctg	tac	aac	atc	tgt	ttc	aga	cat		240
Asn	Gln	Asp	Gly	Phe	Tyr	Tyr	Leu	Tyr	Ala	Asn	Ile	Cys	Phe	Arg	His	
65															80	
cac	gaa	acc	tct	ggt	tct	gtt	cca	acc	gac	tac	ctg	cag	ctg	atg	gtt	288
His	Glu	Thr	Ser	Gly	Ser	Val	Pro	Thr	Asp	Tyr	Leu	Gln	Leu	Met	Val	
85															95	
tac	gtt	gtt	aaa	acc	tct	atc	aaa	atc	cca	tct	tca	cat	aac	ctg	atg	336
Tyr	Val	Val	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His	Asn	Leu	Met	
100															110	
aaa	ggt	ggt	tct	acc	aaa	aac	tgg	tct	ggt	aac	tct	gaa	ttc	cat	ttc	384
Lys	Gly	Gly	Ser	Thr	Lys	Asn	Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	Phe	
115															125	
tac	tct	atc	aac	gtt	ggt	ttc	ttc	aaa	ctg	aga	gct	ggt	gaa	gaa		432
Tyr	Ser	Ile	Asn	Val	Gly	Gly	Phe	Phe	Lys	Leu	Arg	Ala	Gly	Glu	Glu	
130															140	
atc	tct	atc	cag	gtt	tct	aac	cct	tct	ctg	ctg	gac	cca	gac	cag	gac	480
Ile	Ser	Ile	Gln	Val	Ser	Asn	Pro	Ser	Leu	Leu	Asp	Pro	Asp	Gln	Asp	
145															160	
gct	acc	tac	ttc	ggg	gcc	ttc	aaa	gtt	cag	gac	atc	gac				519
Ala	Thr	Tyr	Phe	Gly	Ala	Phe	Lys	Val	Gln	Asp	Ile	Asp				
165															170	

<210> 10

<211> 173

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA encoding
murine OPGL, residues 158-316, fused to His tag

<400> 10

Met	Lys	His	Gln	Lys	Pro											
1														15		
Glu	Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Ser	Ile	Pro		
														30		
Ser	Gly	Ser	His	Lys	Val	Thr	Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly	
														45		
Trp	Ala	Lys	Ile	Ser	Asn	Met	Thr	Leu	Ser	Asn	Gly	Lys	Leu	Arg	Val	
														60		
Asn	Gln	Asp	Gly	Phe	Tyr	Tyr	Leu	Tyr	Ala	Asn	Ile	Cys	Phe	Arg	His	
														80		
His	Glu	Thr	Ser	Gly	Ser	Val	Pro	Thr	Asp	Tyr	Leu	Gln	Leu	Met	Val	
														95		
Tyr	Val	Val	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His	Asn	Leu	Met	
														110		
Lys	Gly	Gly	Ser	Thr	Lys	Asn	Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	Phe	
														125		
115																
120																

Tyr	Ser	Ile	Asn	Val	Gly	Gly	Phe	Phe	Lys	Leu	Arg	Ala	Gly	Glu	Glu
130					135					140					
Ile	Ser	Ile	Gln	Val	Ser	Asn	Pro	Ser	Leu	Leu	Asp	Pro	Asp	Gln	Asp
145					150					155				160	
Ala	Thr	Tyr	Phe	Gly	Ala	Phe	Lys	Val	Gln	Asp	Ile	Asp			
					165					170					

<210> 11
<211> 519
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion of murine OPGL, residues 158-316 with C to S mutation, and His tag

<220>
<221> CDS
<222> (1)..(519)

<220>
<221> misc_binding
<222> (1)..(42)
<223> His tag

<220>
<221> misc_feature
<222> (43)..(228)
<223> Murine OPGL, residues 158-219

<220>
<221> misc_feature
<222> (232)..(519)
<223> Murine OPGL, residues 221-316

<220>
<221> mutation
<222> (229)..(231)
<223> tgt (Cys) to tcc (Ser)

<220>

<400> 11																
atg	aaa	cac	caa	cac	caa	cat	caa	cat	caa	cat	caa	aaa	cct	48		
Met	Lys	His	Gln	His	Pro											
1		5				10						15				
gaa	gct	cag	cca	ttc	gct	cat	ctg	acc	atc	aac	gct	gca	tcg	atc	96	
Glu	Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Ala	Ser	Ile	Pro	
						20		25				30				
tct	ggg	tct	cat	aaa	gtt	acc	ctg	tct	tct	tgg	tat	cac	gac	cgc	144	
Ser	Gly	Ser	His	Lys	Val	Thr	Leu	Ser	Ser	Trp	Tyr	His	Asp.	Arg	Gly	
						35		40			45					
tgg	gct	aaa	atc	tct	aac	atg	acc	ctg	tct	aac	ggg	aaa	ctg	aga	gtt	192
Trp	Ala	Lys	Ile	Ser	Asn	Met	Thr	Leu	Ser	Asn	Gly	Lys	Leu	Arg	Val	
						50		55			60					

aac cag gac ggt ttc tac tac ctg tac gct aac atc tcc ttc aga cat	240
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Ser Phe Arg His	
65 70 75 80	
cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt	288
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val	
85 90 95	
tac gtt gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg	336
Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met	
100 105 110	
aaa ggt ggt tct acc aaa aac tgg tct ggt aac tct gaa ttc cat ttc	384
Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe	
115 120 125	
tac tct atc aac gtt ggt ttc ttc aaa ctg aga gct ggt gaa gaa	432
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu	
130 135 140	
atc tct atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac	480
Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp	
145 150 155 160	
gct acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac	519
Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp	
165 170	

<210> 12
<211> 173
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion of murine OPGL, residues 158-316 with C to S mutation, and His tag

<400> 12	
Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro	
1 5 10 15	
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro	
20 25 30	
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly	
35 40 45	
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val	
50 55 60	
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Ser Phe Arg His	
65 70 75 80	
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val	
85 90 95	
Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met	
100 105 110	
Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe	
115 120 125	
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu	
130 135 140	
Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp	
145 150 155 160	
Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp	
165 170	

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<210> 13
<211> 564
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion of
      murine OPGL, residues 158-316 modified by
      introduction of tetanus toxoid P30 epitope, and
      His tag

<220>
<221> CDS
<222> (1)..(564)

<220>
<221> misc_binding
<222> (1)..(42)
<223> His tag

<220>
<221> misc_feature
<222> (43)..(336)
<223> Murine OPGL, residues 158-255

<220>
<221> misc_feature
<222> (337)..(399)
<223> Tetanus toxoid P30 epitope

<220>
<221> misc_feature
<222> (400)..(564)
<223> Murine OPGL, residues 262-316

<400> 13
atg aaa cac caa cac caa cat caa cat caa cat caa aaa cct      48
Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro
   1           5           10          15
gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct      96
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
   20          25          30
tct ggt tct cat aaa gtt acc ctg tct tgg tat cac gac cgc ggt     144
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
   35          40          45
tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt     192
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
   50          55          60
aac cag gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aga cat     240
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
   65          70          75          80
cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt     288
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
   85          90          95
tac gtt gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg     336
Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met

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100	105	110	
ttc aac aac ttc acc gtt tct ttc tgg ctg agg gta ccg aaa gtt tct	Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser		384
115	120	125	
gct tct cac ctg gaa aac tgg tct ggt aac tct gaa ttc cat ttc tac	Ala Ser His Leu Glu Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr		432
130	135	140	
tct atc aac gtt ggt ttc ttc aaa ctg aga gct ggt gaa gaa atc	Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile		480
145	150	155	160
tct atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac gct	Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala		528
165	170	175	
acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac	Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp		564
180	185		

<210> 14
<211> 188
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion of murine OPGL, residues 158-316 modified by introduction of tetanus toxoid P30 epitope, and His tag

<400> 14			
Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro			
1	5	10	15
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro			
20	25	30	
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly			
35	40	45	
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val			
50	55	60	
Asn Gln Asp Gly Phe Tyr Tyr Ala Asn Ile Cys Phe Arg His			
65	70	75	80
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val			
85	90	95	
Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met			
100	105	110	
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser			
115	120	125	
Ala Ser His Leu Glu Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr			
130	135	140	
Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile			
145	150	155	160
Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala			
165	170	175	
Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp			
180	185		

<210> 15

<211> 546
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion
 between murine OPGL, residues 158-316 with tetanus
 toxoid P2 epitope introduced, and His tag

<220>
 <221> CDS
 <222> (1)..(546)

<220>
 <221> misc_binding
 <222> (1)..(42)
 <223> His tag

<220>
 <221> misc_feature
 <222> (43)..(336)
 <223> Murine OPGL, residues 158-255

<220>
 <221> misc_feature
 <222> (382)..(546)
 <223> Murine OPGL, residues 262-316

<220>
 <221> misc_feature
 <222> (337)..(381)
 <223> Tetanus toxoid P2 epitope

<400> 15		
atg aaa cac caa cac caa cat caa cat caa cat caa aaa cct	48	
Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro		
1 5 10 15		
gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct	96	
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro		
20 25 30		
tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt	144	
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly		
35 40 45		
tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt	192	
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val		
50 55 60		
aac cag gac ggt ttc tac ctg tac gct aac atc tgt ttc aga cat	240	
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His		
65 70 75 80		
cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt	288	
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val		
85 90 95		
tac gtt gtt aaa acc cct atc aaa atc caa tct tca cat aac ctg atg	336	
Tyr Val Val Lys Thr Pro Ile Lys Ile Gln Ser Ser His Asn Leu Met		
100 105 110		
cag tac atc aaa gct aat tcg aaa ttc atc ggt atc acc gaa ctg aac	384	
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Asn		

115	120	125	
tgg tct ggt aac tct gaa ttc cat ttc tac tct atc aac gtt ggt ggt			432
Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly			
130	135	140	
ttc ttc aaa ctg aga gct ggt gaa gaa atc tct atc cag gtt tct aac			480
Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn			
145	150	155	160
cct tct ctg ctg gac cca gac cag gac gct acc tac ttc ggg gcc ttc			528
Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe			
165	170	175	
aaa gtt cag gac atc gac			546
Lys Val Gln Asp Ile Asp			
180			

<210> 16
<211> 182
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
between murine OPGL, residues 158-316 with tetanus
toxoid P2 epitope introduced, and His tag

<400> 16			
Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro			
1	5	10	15
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro			
20	25	30	
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly			
35	40	45	
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val			
50	55	60	
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His			
65	70	75	80
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val			
85	90	95	
Tyr Val Val Lys Thr Pro Ile Lys Ile Gln Ser Ser His Asn Leu Met			
100	105	110	
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Asn			
115	120	125	
Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly			
130	135	140	
Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn			
145	150	155	160
Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe			
165	170	175	
Lys Val Gln Asp Ile Asp			
180			

<210> 17
<211> 519
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion between
 murine OPGL, residues 158-316 with tetanus toxoid
 P2 epitope introduced, and His tag

<220>
 <221> CDS
 <222> (1)..(519)

<220>
 <221> misc_binding
 <222> (1)..(42)
 <223> His tag

<220>
 <221> misc_feature
 <222> (43)..(432)
 <223> Murine OPGL, residues 158-287

<220>
 <221> misc_feature
 <222> (478)..(519)
 <223> Murine OPGL, residues 303-316

<220>
 <221> misc_feature
 <222> (433)..(477)
 <223> Tetanus toxoid P2 epitope

<400> 17

atg	aaa	cac	caa	cac	caa	cat	caa	cat	caa	cat	caa	aaa	cct	48		
Met	Lys	His	Gln	His	Lys	Pro										
1		5				10							15			
gaa	gct	cag	cca	ttc	gct	cat	ctg	acc	atc	aac	gct	gca	tcg	atc	cct	96
Glu	Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Ala	Ser	Ile	Pro	
20						25							30			
tct	ggt	tct	cat	aaa	gtt	acc	ctg	tct	tct	tgg	tat	cac	gac	cgc	ggt	144
Ser	Gly	Ser	His	Lys	Val	Thr	Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly	
35					40							45				
tgg	gct	aaa	atc	tct	aac	atg	acc	ctg	tct	aac	ggt	aaa	ctg	aga	gtt	192
Trp	Ala	Lys	Ile	Ser	Asn	Met	Thr	Leu	Ser	Asn	Gly	Lys	Leu	Arg	Val	
50					55			60								
aac	cag	gac	ggt	ttc	tac	tac	ctg	tac	gct	aac	atc	tgt	ttc	aga	cat	240
Asn	Gln	Asp	Gly	Phe	Tyr	Tyr	Leu	Tyr	Ala	Asn	Ile	Cys	Phe	Arg	His	
65					70			75			80					
cac	gaa	acc	tct	ggt	tct	gtt	cca	acc	gac	tac	ctg	cag	ctg	atg	ggt	288
His	Glu	Thr	Ser	Gly	Ser	Val	Pro	Thr	Asp	Tyr	Leu	Gln	Leu	Met	Val	
85					90			95								
tac	gtt	aaa	acc	tct	atc	aaa	atc	cca	tct	tca	cat	aac	ctg	atg	336	
Tyr	Val	Val	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His	Asn	Leu	Met	
100					105			110								
aaa	ggt	ggt	tct	acc	aaa	aac	tgg	tct	ggt	aac	tct	gaa	ttc	cat	ttc	384
Lys	Gly	Gly	Ser	Thr	Lys	Asn	Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	Phe	
115					120			125								
tac	tct	atc	aac	gtt	ggt	ttc	ttc	aaa	ctg	aga	gct	ggt	gaa	gaa	432	
Tyr	Ser	Ile	Asn	Val	Gly	Gly	Phe	Phe	Lys	Leu	Arg	Ala	Gly	Glu	Glu	
130					135			140								

cag tac atc aaa gct aat tcg aaa ttc atc ggt atc acc gaa ctg gac 480
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Asp
145 150 155 160
gct acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac 519
Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
165 170

<210> 18
<211> 173
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion between
murine OPGL, residues 158-316 with tetanus toxoid
P2 epitope introduced, and His tag

<400> 18
Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro
1 5 10 15
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
20 25 30
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
35 40 45
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
50 55 60
Asn Gln Asp Gly Phe Tyr Tyr Ala Asn Ile Cys Phe Arg His
65 70 75 80
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
85 90 95
Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
100 105 110
Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
115 120 125
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu
130 135 140
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Asp
145 150 155 160
Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
165 170

<210> 19
<211> 519
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion between
murine OPGL, residues 158-316 with tetanus toxoid
P30 epitope introduced, and His tag

<220>
<221> CDS
<222> (1)..(519)

<220>
 <221> misc_binding
 <222> (1)..(42)
 <223> His tag

<220>
 <221> misc_feature
 <222> (43)..(231)
 <223> Murine OPGL, residues 158-220

<220>
 <221> misc_feature
 <222> (295)..(519)
 <223> Murine OPGL, residues 242-316

<220>
 <221> misc_feature
 <222> (232)..(294)
 <223> Tetanus toxoid P30 epitope

<400> 19

atg	aaa	cac	caa	cac	caa	cat	caa	cat	caa	cat	caa	aaa	cct		48	
Met	Lys	His	Gln	Lys	Pro											
1		5				10						15				
gaa	gct	cag	cca	ttc	gct	cat	ctg	acc	atc	aac	gct	gca	tcg	atc	cct	96
Glu	Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Ala	Ser	Ile	Pro	
						20		25					30			
tct	ggt	tct	cat	aaa	gtt	acc	ctg	tct	tgg	tat	cac	gac	cgc	ggt		144
Ser	Gly	Ser	His	Lys	Val	Thr	Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly	
						35		40				45				
tgg	gct	aaa	atc	tct	aac	atg	acc	ctg	tct	aac	ggt	aaa	ctg	aga	gtt	192
Trp	Ala	Lys	Ile	Ser	Asn	Met	Thr	Leu	Ser	Asn	Gly	Lys	Leu	Arg	Val	
						50		55				60				
aac	cag	gac	ggt	ttc	tac	ctg	tac	gct	aac	atc	tgt	ttc	aac	aac		240
Asn	Gln	Asp	Gly	Phe	Tyr	Tyr	Leu	Tyr	Ala	Asn	Ile	Cys	Phe	Asn	Asn	
						65		70			75		80			
ttc	acc	gtt	tct	ttc	tgg	ctg	agg	gta	ccg	aaa	ggt	tct	gct	tct	cac	288
Phe	Thr	Val	Ser	Phe	Trp	Leu	Arg	Val	Pro	Lys	Val	Ser	Ala	Ser	His	
						85		90			95					
ctg	gaa	gtt	aaa	acc	tct	atc	aaa	atc	cca	tct	tca	cat	aac	ctg	atg	336
Leu	Glu	Val	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His	Asn	Leu	Met	
						100		105			110					
aaa	ggt	gtt	tct	acc	aaa	aac	tgg	tct	ggt	aac	tct	gaa	ttc	cat	ttc	384
Lys	Gly	Gly	Ser	Thr	Lys	Asn	Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	Phe	
						115		120			125					
tac	tct	atc	aac	gtt	ggt	ttc	ttc	aaa	ctg	aga	gct	ggt	gaa	gaa		432
Tyr	Ser	Ile	Asn	Val	Gly	Gly	Phe	Phe	Lys	Leu	Arg	Ala	Gly	Glu	Glu	
						130		135			140					
atc	tct	atc	cag	gtt	tct	aac	cct	tct	ctg	ctg	gac	cca	gac	cag	gac	480
Ile	Ser	Ile	Gln	Val	Ser	Asn	Pro	Ser	Leu	Leu	Asp	Pro	Asp	Gln	Asp	
						145		150			155		160			
gct	acc	tac	ttc	ggg	gcc	ttc	aaa	gtt	cag	gac	atc	gac				519
Ala	Thr	Tyr	Phe	Gly	Ala	Phe	Lys	Val	Gln	Asp	Ile	Asp				
						165		170								

<210> 20

<211> 173
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion between murine OPGL, residues 158-316 with tetanus toxoid P30 epitope introduced, and His tag

<400> 20
Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro
1 5 10 15
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
20 25 30
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
35 40 45
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
50 55 60
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Asn Asn
65 70 75 80
Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His
85 90 95
Leu Glu Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
100 105 110
Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
115 120 125
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu
130 135 140
Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
145 150 155 160
Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
165 170

<210> 21
<211> 68
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 21
agctgcagg agtcgggtgg aacagaacca gaggtttcgt gatgtctgaa acagatgtta 60
gcgtacag 68

<210> 22
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 22
ctcatctgac catcaacgct gcat 24

<210> 23
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 23
tttcggtacc ctcagccaga aagaaacggt gaagttgttg aaacagatgt tagcgtacag 60
gttag 64

<210> 24
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 24
tgagggtacc gaaagttct gcttctcacc tggaagttaa aaccctatac aaaatccaat 60
c 61

<210> 25
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 25
tttcggtacc ctcagccaga aagaaacggt gaagttgttg aacatcaggt tatgtgaaga 60
ttg 63

<210> 26
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 26
tgagggtacc gaaagttct gcttctcacc tgaaaaactg gtctggtaac tctgaattcc 60

<210> 27
<211> 79
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR
primer

<400> 27
tacctgcagc ttaggttta cgttgtaaa acccstatca aaatccaatc ttcacataac 60
ctgatgcagt acatcaaag 79

<210> 28
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR
primer

<400> 28
tggaaattcag agttaccaga ccagttcagt tcggtgatac cgatgaattt cgaatttagct 60
ttgatgtact gcatcagggtt atg 83

<210> 29
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR
primer

<400> 29
gaatttcgaa ttagcttga tgtactgttc ttcaccagct cttagttt 49

<210> 30
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR
primer

<400> 30
gctaattcga aattcatcggtatcaccgaa ctggacgcta cctacttcgg ggc 53

<210> 31
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 31
cttactagtc gatgtcctga actttg 26

<210> 32
<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 32
agtggattc agagttacca gaccagttt tggtagaacc acctttcatc agttatgtg 60
aagatggat tttg 74

<210> 33
<211> 65
<212> DNA
<213> Clostridium tetani

<400> 33
actacactgca gctgatggtt tacgttgtt aaacctctat caaaatccca tcttcacata 60
acctg 65

*a 10
a Cont*

<210> 34
<211> 15
<212> PRT
<213> Clostridium tetani

<400> 34
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
1 5 10 15

<210> 35
<211> 21
<212> PRT
<213> Clostridium tetani

<400> 35
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
1 5 10 15
Ala Ser His Leu Glu
20

<210> 36
<211> 13
<212> PRT
<213> Artificial Sequence

*A¹⁰
Cont*
<220>
<223> A pan DR epitope ("PADRE") peptide

<400> 36
Ala Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala
1 5 10
